

SEQUENCE CHARACTERISTICS:
 LENGTH: 381 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-146-187-2

Query Match 100.0%; Score 1996; DB 4; Length 381;
 Best Local Similarity 100.0%; Pred. No. 2.8e-158;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSKTKYKRDLYVROGVNVIAMTKDKLPVLDYVFNDSGSSRELVLNLTGTFVRYRGNTYNI 60
 1 MMSKTKYKRDLYVROGVNVIAMTKDKLPVLDYVFNDSGSSRELVLNLTGTFVRYRGNTYNI 60
 61 PICMLDLYPNPPICEVKPTSSMTIKTKGHVANGKIYLPYLHDMKHPRSELELQI 120
 61 PICMLDLYPNPPICEVKPTSSMTIKTKGHVANGKIYLPYLHDMKHPRSELELQI 120
 121 MIVFGEPPVFSRPTVSAVPPYATGPPNTSYMPGMSGISAYPSGYPNPGYPCGP 180
 121 MIVFGEPPVFSRPTVSAVPPYATGPPNTSYMPGMSGISAYPSGYPNPGYPCGP 180
 181 YPPAGPYPATSSQYSPQPVTVGSPRDTISEDTIRASLISAVSDKLRRMKEMDGA 240
 181 YPPAGPYPATSSQYSPQPVTVGSPRDTISEDTIRASLISAVSDKLRRMKEMDGA 240
 241 QAEINLAKRTEDLKKGHOKLEMYTRLDQEVAVDNKLTLLKKKDELSALEKMNOS 300
 241 QAEINLAKRTEDLKKGHOKLEMYTRLDQEVAVDNKLTLLKKKDELSALEKMNOS 300
 301 ENNDIDEVLIPTAPLYKQILNLYAEENAIEDTIFYLGEALRGVYIDLVFLKHVLLSRK 360
 301 ENNDIDEVLIPTAPLYKQILNLYAEENAIEDTIFYLGEALRGVYIDLVFLKHVLLSRK 360
 361 QFOLRALMOKARKTAGLSLY 381
 361 QFOLRALMOKARKTAGLSLY 381

RESULT 6
 US-08-585-758A-4

Sequence 4, Application US/08585758A
 Patent No. 5679523
 GENERAL INFORMATION:
 APPLICANT: LI, Limin
 APPLICANT: COHEN, Stanley N.
 TITLE OF INVENTION: METHOD FOR CONCURRENT DISRUPTION OF
 TITLE OF INVENTION: EXPRESSION OF MULTIPLE ALLELES OF MAMMALIAN GENES
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
 STREET: FOUR EMBARCADERO CENTER, SUITE 3400
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/585,758A
 FILING DATE: 12-JAN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertam I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A62783/BIR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 380 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-585-758A-4

Query Match 95.2%; Score 1900.5; DB 1; Length 380;
 Best Local Similarity 94.5%; Pred. No. 2.5e-150;
 Matches 360; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

1 MSKTKYKRDLYVROGVNVIAMTKDKLPVLDYVFNDSGSSRELVLNLTGTFVRYRGNTYNI 60
 1 MMSKTKYKRDLYVROGVNVIAMTKDKLPVLDYVFNDSGSSRELVLNLTGTFVRYRGNTYNI 60
 61 PICMLDLYPNPPICEVKPTSSMTIKTKGHVANGKIYLPYLHDMKHPRSELELQI 120
 61 PICMLDLYPNPPICEVKPTSSMTIKTKGHVANGKIYLPYLHDMKHPRSELELQI 120
 121 MIVFGEPPVFSRPTVSAVPPYATGPPNTSYMPGMSGISAYPSGYPNPGYPCGP 180
 121 MIVFGEPPVFSRPTVSAVPPYATGPPNTSYMPGMSGISAYPSGYPNPGYPCGP 180
 181 YPPAGPYPATSSQYSPQPVTVGSPRDTISEDTIRASLISAVSDKLRRMKEMDGA 240
 181 YPPAGPYPATSSQYSPQPVTVGSPRDTISEDTIRASLISAVSDKLRRMKEMDGA 240
 241 QAEINLAKRTEDLKKGHOKLEMYTRLDQEVAVDNKLTLLKKKDELSALEKMNOS 300
 241 QAEINLAKRTEDLKKGHOKLEMYTRLDQEVAVDNKLTLLKKKDELSALEKMNOS 300
 301 ENNDIDEVLIPTAPLYKQILNLYAEENAIEDTIFYLGEALRGVYIDLVFLKHVLLSRK 360
 301 ENNDIDEVLIPTAPLYKQILNLYAEENAIEDTIFYLGEALRGVYIDLVFLKHVLLSRK 360
 361 QFOLRALMOKARKTAGLSLY 381
 361 QFOLRALMOKARKTAGLSLY 380

RESULT 7

US-08-977-818-4

Sequence 4, Application US/08977818
 Patent No. 5807995
 GENERAL INFORMATION:
 APPLICANT: LI, Limin
 APPLICANT: COHEN, Stanley N.
 TITLE OF INVENTION: MAMMALIAN TUMOR SUSCEPTIBILITY GENES AND
 TITLE OF INVENTION: THEIR USES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH AND RICHARDSON, P.C.
 STREET: 2200 SAND HILL ROAD
 CITY: MENLO PARK
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,818
 FILING DATE: 25-NOV-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/670,274
 FILING DATE: June 13, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: SHERWOOD, Pamela J.
 REGISTRATION NUMBER: 36,677

MOOSE vs. human

RESULT 2

gene CC2 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I48283

R:Maunier, A.; Camonis, J.H.; Sobel, A.

Proc. Natl. Acad. Sci. U.S.A. 92, 3100-3104, 1995

A:Title: Stathmin interaction with a putative kinase and coiled-coil-forming protein domain

A:Reference number: I48282; MUID:95241452; PMID:7724523

A:Accession: I48283

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-83 <RES>

A:Cross-references: EMBL:X82319; NID:g791075; PIDN:CAA57762.1; PID:g791076

C:Genetics:

C:Gene: CC2

Query Match

Best Local Similarity 19.4%; Score 388; DB 2; Length 82; Indels 0; Gaps 0;

Matches 80; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

231 RMKEEDMAQAEALNAKRTEDLKKGHQLKEVNTRLDQEAIVDKKIKKDEELSS 290

DB 1 RMKEEDMAQAEALNAKRTEDLKKGHQLKEVNTRLDQEAIVDKKIKKDEELSS 60

291 ALEKMESENNDIDEVILPTA 312

DB 61 ALEKMESENNDIDEVILPTA 82

RESULT 3

T34520

hypothetical protein DKFZP564J157.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T34520

R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, October 1999

A:Reference number: 221539

A:Accession: T34520

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-169 <BLO>

A:Cross-references: EMBL:AL122042

A:Experimental source: fetal brain; clone DKFZP564J157

C:Genetics:

A:Note: DKFZP564J157.1

Query Match

Best Local Similarity 7.7%; Score 153.5; DB 2; Length 169;

Matches 42; Conservative 18; Mismatches 45; Indels 33; Gaps 6;

126 GDEPPVSRPISASVPPYQATGPPNTSYNPGMPCGISPISGYPNP---SGYPC- 178

DB 43 GGSNAHPPIPPPPPPGPPPP---FGAPGNPAFPSPGPPHPVPPQPPGQPPG 96

179 PYPGPPYATSSQYPPSOPPVTVVGSRDGTISEDTIRASLISAVSDKLRRMKEEMDR 238

DB 97 PYPGPPYATSSQYPPSOPPVTVVGSRDGTISEDTIRASLISAVSDKLRRMKEEMDR 136

239 AQAELNAKRTEDLKKG 256

DB 137 AAKKMKHOKHKKYKRG 154

RESULT 4

L0H07

annexin VII, long form - human

Alternative names: synexin

Contains: annexin VII, long form; annexin VII, short form

Query Match

Best Local Similarity 7.3%; Score 147; DB 1; Length 488;

Matches 89; Conservative 34; Mismatches 88; Indels 200; Gaps 19;

139 SYPPYQATG-PPTSYMPC---MPGISPISGYPNP---SGYPC- 169

DB 2 SYPPYQATG-PPTSYMPC---MPGISPISGYPNP---SGYPC- 61

170 PNPISGYPNP---SGYPC- 204

DB 62 APGGYPAPGGYGAPOGGAPSPVPGVPPGAGGSGIP-QPPSGYGGGPPAGY 120

205 PNPISGYPNP---SGYPC- 217

DB 121 PNPISGYPNP---SGYPC- 180

218 PNPISGYPNP---SGYPC- 254

DB 181 PNPISGYPNP---SGYPC- 240

255 K---SGYPC- 274

WEST**Create A Case**

Select?	Database	Query	Plural	Op	Thesaurus	Set Name
<input checked="" type="checkbox"/>	USPT,JPAB,EPAB	tsg101	YES	ADJ	ASSIGNEE	L1
<input checked="" type="checkbox"/>	USPT,JPAB,EPAB	L1 and antibody	YES	ADJ	ASSIGNEE	L2
<input checked="" type="checkbox"/>	USPT,JPAB,EPAB	L2 and (normal or wild)	YES	ADJ	ASSIGNEE	L3

Please enter the case name:

Rules for naming Cases

- Case names can only contain alphanumeric characters including underscore (_).
- Any other special characters or punctuation characters will be automatically removed prior to saving the case.
- All white space characters will be replaced by an underscore.

WEST

Generate Collection

Print

L3: Entry 15 of 16

File: USPT

Sep 15, 1998

US-PAT-NO: 5807995

DOCUMENT-IDENTIFIER: US 5807995 A

**** See image for Certificate of Correction ****

TITLE: Mammalian tumor susceptibility genes and their uses

DATE-ISSUED: September 15, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cohen; Stanley N.	Stanford	CA		
Li; Limin	Stanford	CA		

US-CL-CURRENT: 530/350

CLAIMS:

What is claimed is:

1. A purified polypeptide composition comprising at least 50 weight % of the protein present as a TSG101 protein or a fragment thereof.
2. A purified polypeptide composition according to claim 1, wherein said TSG101 protein is a mammalian protein.
3. A purified polypeptide composition according to claim 2, wherein said TSG101 protein is a human protein.
4. A purified polypeptide composition according to claim 2, wherein said TSG101 protein is a mouse protein.

Your SELECT statement is:
s tsg101

Items	File
91	5: Biosis Previews(R) 1969-2003/May W4
102	34: SciSearch(R) Cited Ref Sci 1990-2003/May W4
5	35: Dissertation Abs Online 1861-2003/May
10	65: Inside Conferences 1993-2003/Jun W1
74	71: ELSEVIER BIOBASE 1994-2003/Jun W1
76	73: EMBASE 1974-2003/May W4
2	94: JICST-EPlus 1985-2003/Jun W1
14	98: General Sci Abs/Full-Text 1984-2003/Apr
9	135: NewsRx Weekly Reports 1995-2003/May W4
38	144: Pascal 1973-2003/May W4
23	149: TGG Health&Wellness DB(SM) 1976-2003/May W4
93	155: MEDLINE(R) 1966-2003/May W4
12	156: ToxFile 1965-2003/May W4
58	159: Cancerlit 1975-2002/Oct
3	162: Global Health 1983-2003/Apr
9	172: EMBASE Alert 2003/Jun W1
5	266: FEDRIP 2003/Apr
89	399: CA SEARCH(R) 1967-2003/UD=13823

File 5:Biosis Previews(R) 1969-2003/May W4
(c) 2003 BIOSIS

***File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.**

File 34:SciSearch(R) Cited Ref Sci 1990-2003/May W4
(c) 2003 Inst for Sci Info

***File 34: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.**

File 155:MEDLINE(R) 1966-2003/May W4
(c) format only 2003 The Dialog Corp.

***File 155: Medline has been reloaded and accession numbers have changed. Please see HELP NEWS 155.**

File 58:GeoArchive 1974-2003/Apr
(c) 2003 Geosystems

File 89:GeoRef 1785-2003/Jun B1
(c) 2003 American Geological Institute

***File 89: Truncate SH codes for a complete retrieval.Set** Items Description

S1	286	TSG101
S2	1	S1 NOT PY=>1996
S3	1	RD (unique items)

3/9/1 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

08553152 95241452 PMID: 7724523

Stathmin interaction with a putative kinase and coiled-coil-forming protein domains.

Maucuer A; Camonis J H; Sobel A
Institut National de la Sante et de la Recherche Medicale, Unite 153,
Paris, France.

Proceedings of the National Academy of Sciences of the United States of
America (UNITED STATES) Apr 11 1995, 92 (8) p3100-4, ISSN 0027-8424
Journal Code: 7505876

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Stathmin is a ubiquitous, cytosolic 19-kDa protein, which is phosphorylated on up to four sites in response to many regulatory signals within cells. Its molecular characterization indicates a functional organization including an N-terminal regulatory domain that bears the phosphorylation sites, linked to a putative alpha-helical binding domain predicted to participate in coiled-coil, protein-protein interactions. We therefore proposed that stathmin may play the role of a relay integrating diverse intracellular regulatory pathways; its action on various target

proteins would be a function of its combined phosphorylation state. To search for such target proteins, we used the two-hybrid screen in yeast, with stathmin as a "bait." We isolated and characterized four cDNAs encoding protein domains that interact with stathmin in vivo. One of the corresponding proteins was identified as BiP, a member of the hsp70 heat-shock protein family. Another is a previously unidentified, putative serine/threonine kinase, KIS, which might be regulated by stathmin or, more likely, be part of the kinases controlling its phosphorylation state. Finally, two clones code for subdomains of two proteins, CC1 and CC2, predicted to form alpha-helices participating in coiled-coil interacting structures. Their isolation by interaction screening further supports our model for the regulatory function of stathmin through coiled-coil interactions with diverse downstream targets via its presumed alpha-helical binding domain. The molecular and biological characterization of KIS, CC1, and CC2 proteins will give further insights into the molecular functions and mechanisms of action of stathmin as a relay of integrated intracellular regulatory pathways.

= TSG101

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--metabolism--ME; *Heat-Shock Proteins 70--metabolism--ME; *Phosphoproteins--metabolism--ME; *Protein Structure, Tertiary; *Protein-Serine-Threonine Kinases--metabolism--ME; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Base Sequence; Heat-Shock Proteins 70--genetics--GE; Mice; Molecular Sequence Data; Phosphoproteins--genetics--GE; Protein Binding; Protein-Serine-Threonine Kinases--genetics--GE; Proteins--metabolism--ME; Recombinant Fusion Proteins--metabolism--ME; Saccharomyces cerevisiae--genetics--GE; Sequence Homology, Amino Acid; Signal Transduction--genetics--GE; Tissue Distribution

Molecular Sequence Databank No.: GENBANK/X82318; GENBANK/X82319; GENBANK/X82320

CAS Registry No.: 0 (Bacterial Proteins); 0 (Heat-Shock Proteins 70); 0 (Kis protein); 0 (Phosphoproteins); 0 (Proteins); 0 (Recombinant Fusion Proteins); 0 (Tsg101 protein); 0 (coiled-coil-forming protein 1); 0 (stathmin)

Enzyme No.: EC 2.7.1.- (protein kinase KIS); EC 2.7.1.37 (Protein-Serine-Threonine Kinases)

Yu, Misook

To: Chan, Christina
Subject: 09804690

the case is due this biweek. Please approve rush search for SEQ IS NO:2 and 4. They are both proteins with 380 aa.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 95625

To: Misook Yu
Location: CM1-8E12
Art Unit: 1642
Tuesday, June 03, 2003

Case Serial Number: 09/804690

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes